

## IT IS CLAIMED:

1. A method for identifying genes associated with a desired trait in a fruit-bearing plant comprising.

(i) transforming cells of a plant with a plant cell expression vector having an *E. coli* origin of replication, an element which functions to enhance gene expression, a selectable marker-encoding nucleotide sequence operably linked to a promoter effective to express the selectable marker encoding sequence, a termination element for said selectable marker-encoding nucleotide sequence, and a T-DNA sequence;

(ii) in a manner effective to express said selectable marker-encoding nucleotide sequence;

(ii) selecting plant cells which have been transformed by their ability to grow in the presence of an amount of selective agent that is toxic to non-transformed plant cells;

(iii) regenerating transformed plant cells to yield mature plants;

(iv) selecting plants having a desired trait; and

(v) identifying, isolating and characterizing genes the transcription of which was enhanced by said element which functions to enhance gene expression.

2. The method of claim 1, further comprising the steps of

(vi) preparing a separate heterologous gene construct for each isolated gene;

(vii) transforming plants with said separate heterologous gene construct in a manner effective to enhance expression of the isolated gene in said plants;

(vii) selecting plants having the desired trait.

3. The method of claim 1, wherein the element which functions to enhance gene expression is selected from the group consisting of a CaMV 35S enhancer element, a Figwort Mosaic Virus (FMV) promoter sequence, a peanut chlorotic streak caulimovirus full-length transcript (PCISVFLt) sequence and a mirabilis mosaic virus (MMV), promoter sequence (SEQ ID NO:8).

4. The method of claim 2, wherein said CaMV 35S enhancer element is a 4X tandem duplicated CaMV 35S enhancer element having the sequence presented as SEQ ID NO:1.

5. The method of claim 2, wherein said Figwort Mosaic Virus (FMV) sequence is the promoter sequence presented as SEQ ID NO:5 or the enhancer sequence presented as SEQ ID NO:6.

6. The method of claim 2, wherein said peanut chlorotic streak caulimovirus full-length transcript (PCISVFLt) sequence is the enhancer sequence presented as SEQ ID NO:7.

7. The method of claim 2, wherein said mirabilis mosaic virus (MMV) sequence is the promoter sequence presented as SEQ ID NO:8.

8. The method of claim 1, wherein said selectable marker is a polypeptide which confers herbicide-resistance to transformed plant cells expressing said marker.

9. The method of claim 1, wherein said selectable marker is an antibiotic resistance gene which confers resistance to an antibiotic selected from the group consisting of kanamycin, G418, bleomycin, hygromycin, chloramphenicol, ampicillin and tetracycline.

10. The method of claim 8, wherein said antibiotic is kanamycin.

11. The method of claim 1, wherein said fruit-bearing plant is a dwarf plant.

12. The method of claim 10, wherein said dwarf plant is a tomato plant.

13. The method of claim 1, wherein said transforming cells includes *Agrobacterium tumefaciens*-mediated transformation.

14. The method of claim 12, wherein said transforming cells includes introduction of *Agrobacterium tumefaciens* into hypocotyl tissue derived from said fruit-bearing plant.

15. The method of claim 12, wherein said transforming cells includes introduction of *Agrobacterium tumefaciens* into shoot tip tissue derived from said fruit-bearing plant.

16. The method of claim 1, wherein said desired trait is a biochemical modification of a plant and fruit selected from the group consisting of a change in the level of vitamins, a change in the level of minerals, or elements, a change in the level of amino acids, a change in the level of carbohydrates, a change in the level of lipids, a change in the level of nitrogenous bases, a change in the level of isoprenoids, a change in the level of phenylpropanoids and a change in the level of alkaloids.

17. The method of claim 1, wherein said desired trait is a fruit-bearing plant specific trait selected from the group consisting of increased resistance to fungal, bacterial or viral pathogens, increased resistance to insects, modified flower size, modified flower number, modified flower pigmentation and shape, modified leaf number, modified leaf pigmentation and shape, modified seed number, a modified pattern or distribution of leaves and flowers, modified stem length between nodes, modified root mass or root development characteristics, and increased drought, salt and antibiotic tolerance.

18. The method of claim 1, wherein said plant cell expression vector is selected from the group consisting of pSKI15, pAG 3201, pAG 3202 and pAG 4201.

19. A transgenic fruit-bearing plant comprising enhanced expression of a gene identified by the method of claim claim 1, 16 or 17.